###DISSIMILARITY MATRICES + MANTEL CORRELATION----------------------

##import data

spe <- read.delim("forest\_JMK\_species.txt", header=T, row.names=1)

#standardize to presence/absence data

#library(vegan)

spe.pa <- decostand(spe, "pa")

spe.pa[1:10,1:10]

#calculate dissimilarity matrices

beta.j <- vegdist(spe.pa, method = "jaccard")

head(beta.j)

class(beta.j)

#convert to matrix

beta.j.mat <- as.matrix(beta.j)

beta.j.mat[1:5,1:5]

betadiver(help=TRUE)

beta.b <- betadiver(spe.pa, method = "sim")

#calculate environmental and geographical distances

coord <- forest[, c("X", "Y")]

geodist <- dist(coord, method = "euclidean")

envdist <- dist(env.tab.s, method = "euclidean")

#mantel correlation

m.geo <- mantel(beta.b, geodist, permutations=499)

m.env <- mantel(beta.b, envdist, permutations=499)

#plot relationship

plot(geodist, beta.b)

plot(envdist, beta.b)

plot.data <- cbind(envdist, beta.b)

plot(plot.data, col = densCols(plot.data, colramp = colorRampPalette(c("gray90", "gray10"))))